Amendments to the Specification:

On page 9 please delete the paragraph beginning on line 15, and replace it with the following:

--**Figure 5A.** Sequence alteration within variable chain of an antibody (a mutation within the light chain variable region in MMR-defective HB134 antibody producer cells). Arrows indicate the nucleotide at which a mutation occurred in a subset of cells from a clone derived from HB134 cells. The HB134 sequence (SEQ ID NO:19) is shown as the top line and the parental H36 sequence (SEQ ID NO:20) is shown above and below the sequence tracing. ~~Panel A:~~ The change results in a Thr to Ser change within the light chain variable region. The coding sequence is in the antisense direction. ~~Panel B:~~

Figure 5B. Sequence alteration within variable chain of an antibody (a mutation within the light chain variable region in MMR-defective HB134 antibody producer cells). The HB134 sequence (SEQ ID NO:21) is shown above and below the tracing for the HB134 sequence, and the parental H36 sequence (SEQ ID NO:22) is shown above and below the H36 sequence tracing. A consensus sequence (SEQ ID NO:23) is shown at the bottom of the figure. Arrows indicate the nucleotide at which a mutation occurred in a subset of cells from a clone derived from HB134 cells. The change results in a Pro to ~~His~~ Leu change within the light chain variable region.--

On page 30, please replace the paragraph beginning on line 12 with the following:

--PCR reactions using degenerate oligonucleotides are carried out at 94°C for 30 sec, 52°C for 1 min, and 72°C for 1 min for 35 cycles. Products are analyzed on agarose gels. Products of the expected molecular weights are purified from the gels by Gene Clean (Bio

101), cloned into T-tailed vectors, and sequenced to identify the wild type sequence of the variable light and heavy chains. Once the wild type sequence has been determined, non-degenerate primers were made for RT-PCR amplification of positive HB134 clones. Both the light and heavy chains were amplified, gel purified and sequenced using the corresponding sense and antisense primers. The sequencing of RT-PCR products gives representative sequence data of the endogenous immunoglobulin gene and not due to PCR induced mutations. Sequences from clones were then compared to the wild type sequence for sequence comparison. An example of the ability to create *in vivo* mutations within an immunoglobulin light or heavy chain is shown in figure 5, where HB134 clone92 was identified by ELISA to have an increased signal for hIgE. The light chain was amplified using specific sense and antisense primers. The light chain was RT-PCR amplified and the resulting product was purified and analyzed on an automated ABI377 sequencer. As shown in clone A, a residue –4 upstream of the CDR region 3 had a genetic change from ACT to TCT, which results in a Thr to Ser change within the framework region just preceding the CDR#3. In clone B, a residue –6 upstream of the CDR region had a genetic change from CCC to CTC, which ~~reslts~~ results in a Pro to ~~His~~ Leu change within framework region ~~preceeding~~ preceding CDR#2.--

Please replace the Sequence Listing currently on file with the enclosed Substitute Sequence Listing.

Amendments to the Drawings

The attached sheet(s) of drawings includes changes to Fig(s) 1, 2, 3, 4, 5A, 5B, and 6. The sheet(s), which includes Fig(s) 1, 2, 3, 4, 5A, 5B, and 6, replaces the original sheet(s) including Fig(s) 1, 2, 3, 4, 5A, 5B, and 6.

Attachment: Replacement Sheet(s)